

CLAIMS LISTING

1. (Currently Amended) A method of analyzing gene expressions comprising acts of:
 - 5 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;
 - forming a first spatial-expression pattern by:
 - selecting a chromosomal region having a length and an exon having a start and a stop position; and
 - associating the gene expression within the first gene expression pattern with its corresponding exon by: , the corresponding exon having a length such that the gene expression is associated with the entire length of the corresponding exon.
 - 10 determining, within the chromosomal region, the start and stop position of the exon; and
 - 15 associating the gene expression to the first-spatial expression pattern for the length between the start and stop position of the exon.
2. (Original) The method of claim 1, wherein:
 - 20 the act of forming the first spatial-expression pattern further comprises an act of creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.
- 25 3. (Original) The method of claim 2, wherein:
 - the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.
- 30 4. (Original) The method of claim 2, further comprising an act of:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

5. (Withdrawn) The method of claim 4, wherein

5 the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

6. (Withdrawn) The method of claim 5, further comprising an act of:

10 identifying a group of genes contributing to local maximum points of the generated Fourier transform spectrum.

7. (Original) The method of claim 4, wherein

15 the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

8. (Original) The method of claim 7, further comprising an act of:

identifying a group of genes contributing to local maximum points of the generated Wavelet transformed signal at different scales and positions.

20 9. (Original) The method of claim 4, wherein:

the act of identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes.

10. (Original) The method of claim 9, wherein:

25 the act of identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes which participate in a common biological process or function.

11. (Original) The method of claim 1, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

5 associating a gene expression within the second gene expression pattern with its corresponding exon.

12. (Original) The method of claim 11, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern

10 signal;

identifying second regular spatial patterns in the second spatial-expression pattern signal; and

comparing the first and second regular spatial patterns.

15 13. (Original) The method of claim 11, further comprising an act of:

repeating the steps of determining a gene expression pattern and forming a spatial-expression pattern signal for any number of gene expression patterns.

14. (Original) The method of claim 13, further comprising acts of:

20 comparing all formed spatial-expression pattern signals.

15. (Original) The method of claim 14, wherein:

the act of comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

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16. (Original) The method of claim 15, further comprising acts of:

identifying gene groups contributing to the differences in significant changes in the first and second regular spatial-expression pattern signals.

17. (Original) The method of claim 1, wherein the chromosomal region is an entire chromosome.

18. (Original) The method of claim 11, wherein:

5 the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

19. (Original) The method of claim 11, wherein:

10 the first spatial-expression and the second-expression pattern are selected from different genomes.

20. (Currently Amended) An apparatus for analyzing gene expressions, the apparatus comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

15 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

 forming a first spatial-expression pattern by:

20 selecting a chromosomal region having a length and an exon having a start and a stop position; and

 associating the gene expression within the first gene expression pattern with its corresponding exon by: the corresponding exon having a length such that the gene expression is associated with the entire length of the corresponding exon.

25 determining, within the chromosomal region, the start and stop position of the exon; and

associating the gene expression to the first-spatial expression pattern for the length between the start and stop position of the exon.

21. (Original) An apparatus as set forth in claim 20, wherein:

the means for forming the first spatial-expression pattern further comprises an
means for creating a first spatial-expression pattern signal wherein the first spatial-
5 expression pattern signal is a representation of the first spatial-expression pattern
where a magnitude of the first spatial-expression pattern signal at any point is
determined by an expression level of the corresponding exon.

22. (Original) An apparatus as set forth in claim 21, wherein:

10 the magnitude of the first spatial-expression pattern signal at points spanning
the chromosomal region are a function of the expression level of an exon at
corresponding positions in the chromosomal region.

23. (Original) An apparatus as set forth in claim 21, further comprising an means for:

15 identifying first regular spatial patterns in the first spatial-expression pattern
signal.

24. (Withdrawn) An apparatus as set forth in claim 23, wherein

20 the means for identifying first regular spatial patterns in the first spatial-
expression pattern signal is performed through the use of Fourier transform signal
processing.

25. (Withdrawn) An apparatus as set forth in claim 24, further comprising an means for:

identifying a group of genes contributing to local maximum points of the
25 generated Fourier transform spectrum.

26. (Original) An apparatus as set forth in claim 23, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

5 27. (Original) An apparatus as set forth in claim 26, further comprising an means for:
identifying a group of genes contributing to local maximum points of the generated Wavelet transformed signal at different scales and positions.

28. (Original) An apparatus as set forth in claim 23, wherein:

10 the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes.

29. (Original) An apparatus as set forth in claim 28, wherein:

15 the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes which participate in a common biological process or function.

30. (Original) An apparatus as set forth in claim 20, further comprising acts of:

20 determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and forming a second spatial-expression pattern by:
selecting a chromosomal region having an exon; and
associating a gene expression within the second gene expression pattern with its corresponding exon.

25 31. (Original) An apparatus as set forth in claim 30, further comprising acts of:
identifying first regular spatial patterns in the first spatial-expression pattern signal;

identifying second regular spatial patterns in the second spatial-expression pattern signal; and

comparing the first and second regular spatial patterns.

5 32. (Original) An apparatus as set forth in claim 31, further comprising an means for:
repeating the steps of determining a gene expression pattern and forming a spatial-expression pattern signal for any number of gene expression patterns.

33. (Original) An apparatus as set forth in claim 30, further comprising acts of:
10 comparing all formed spatial-expression pattern signals.

34. (Original) An apparatus as set forth in claim 33, wherein:
the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

15 35. (Original) An apparatus as set forth in claim 34 further comprising acts of:
identifying gene groups contributing to the differences in significant changes in the first and second regular spatial-expression pattern signals.

20 36. (Original) An apparatus as set forth in claim 20, wherein the chromosomal region is an entire chromosome.

37. (Previously Presented) An apparatus as set forth in claim 30, wherein:
the first spatial-expression pattern and the second-expression pattern are
25 selected from different chromosomes.

38. (Original) An apparatus as set forth in claim 30, wherein:
the first spatial-expression and the second-expression pattern are selected from different genomes.

39. (Currently Amended) A computer program product for analyzing gene expressions, the computer program product comprising means, encoded in a computer-readable medium for:

5 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having a length and an exon having a start and a stop position; and

10 associating the gene expression within the first gene expression pattern with its corresponding exon by: the corresponding exon having a length such that the gene expression is associated with the entire length of the corresponding exon.

determining, within the chromosomal region, the start and

15 stop position of the exon; and

associating the gene expression to the first-spatial expression pattern for the length between the start and stop position of the exon.

20 40. (Original) A computer program product as set forth in claim 39, wherein:

the means for forming the first spatial-expression pattern further comprises a means for creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is

25 determined by an expression level of the corresponding exon.

41. (Original) A computer program product as set forth in claim 40, wherein:

the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

5 42. (Original) A computer program product as set forth in claim 40, further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

10 43. (Withdrawn) A computer program product as set forth in claim 42, wherein the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

15 44. (Withdrawn) A computer program product as set forth in claim 43, further comprising an means for:

identifying a group of genes contributing to local maximum points of the generated Fourier transform spectrum.

20 45. (Original) A computer program product as set forth in claim 42, wherein the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

25 46. (Original) A computer program product as set forth in claim 45, further comprising an means for:

identifying a group of genes contributing to local maximum points of the generated Wavelet transformed signal at different scales and positions.

47. (Original) A computer program product as set forth in claim 42, wherein:
the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes.

5 48. (Original) A computer program product as set forth in claim 47, wherein:
the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes which participate in a common biological process or function.

10 49. (Original) A computer program product as set forth in claim 39, further comprising acts of:
determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and
forming a second spatial-expression pattern by:
15 selecting a chromosomal region having an exon; and
associating a gene expression within the second gene expression pattern with its corresponding exon.

20 50. (Original) A computer program product as set forth in claim 49, further comprising acts of:
identifying first regular spatial patterns in the first spatial-expression pattern signal;
identifying second regular spatial patterns in the second spatial-expression pattern signal; and
25 comparing the first and second regular spatial patterns.

51. (Original) A computer program product as set forth in claim 50, further comprising an means for:

repeating the steps of determining a gene expression pattern and forming a spatial-expression pattern signal for any number of gene expression patterns.

52. (Original) A computer program product as set forth in claim 49, further comprising acts of:

comparing all formed spatial-expression pattern signals.

53. (Original) A computer program product as set forth in claim 52, wherein:

the means for comparing all formed spatial-expression pattern signals

10 involves clustering all formed spatial-expression pattern signals.

54. (Original) A computer program product as set forth in claim 53, further comprising acts of:

identifying gene groups contributing to the differences in significant changes

15 in the first and second regular spatial-expression pattern signals.

55. (Previously Presented) A computer program product as set forth in claim 39, wherein the chromosomal region is an entire chromosome.

20 56. (Original) A computer program product as set forth in claim 39, wherein:

the first spatial-expression pattern and the second-expression pattern are

selected from different chromosomes.

57. (Original) A computer program product as set forth in claim 39, wherein:

25 the first spatial-expression and the second-expression pattern are selected from different genomes.

58. (Currently Amended) A method of analyzing gene expressions comprising acts of:

5 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;
 forming a first spatial-expression pattern by:
 selecting a chromosomal region having a length and an exon having a start and stop position;
 associating the gene expression within the first gene expression pattern with its corresponding exon by: ~~the corresponding exon having a length such that the gene expression is associated with the entire length of the corresponding exon~~;
 determining, within the chromosomal region, the start and stop position of the exon; and
 associating the gene expression to the first-spatial expression pattern for the length between the start and stop position of the exon; and
 creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.
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15 59. (Original) The method of claim 58, further comprising an act of:
 identifying first regular spatial patterns in the first spatial-expression pattern signal.
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25 60. (Withdrawn) The method of claim 59, wherein
 the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.
61. (Original) The method of claim 59, wherein

the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

62. (Original) The method of claim 58, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein
the second gene expression pattern comprises a gene expression; and
forming a second spatial-expression pattern by:

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selecting a chromosomal region having an exon; and
associating a gene expression within the second gene expression pattern
with its corresponding exon.

63. (Original) The method of claim 62, further comprising acts of:

10 identifying first regular spatial patterns in the first spatial-expression pattern
signal;
identifying second regular spatial patterns in the second spatial-expression
pattern signal; and
comparing the first and second regular spatial patterns.

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64. (Original) The method of claim 62, further comprising acts of:

comparing all formed spatial-expression pattern signals.

65. (Original) The method of claim 64, wherein:

20 the act of comparing all formed spatial-expression pattern signals involves
clustering all formed spatial-expression pattern signals.

66. (Currently Amended) An apparatus for analyzing gene expressions, the apparatus
comprising a computer system including a processor, a memory coupled with the
processor, an input coupled with the processor for receiving input data, and an output
coupled with the processor for outputting data, wherein the computer system further
comprises means, residing in its processor and memory, for:

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determining a first gene expression pattern for a first condition, wherein the
first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having a length and an exon having a start and a stop position;

associating the gene expression within the first gene expression pattern

5 with its corresponding exon by: the corresponding exon having a length such that the gene expression is associated with the entire length of the corresponding exon;

determining, within the chromosomal region, the start and stop position of the exon;

associating the gene expression to the first-spatial expression

10 pattern for the length between the start and stop position of the exon; and

creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

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67. (Original) An apparatus as set forth in claim 66, further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

20 68. (Withdrawn) An apparatus as set forth in claim 67, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

25 69. (Original) An apparatus as set forth in claim 67, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

70. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

5 forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern with its corresponding exon.

10 71. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern signal;

15 identifying second regular spatial patterns in the second spatial-expression pattern signal; and

comparing the first and second regular spatial patterns.

72. (Previously Presented) An apparatus as set forth in claim 66, further comprising acts of:

20 comparing all formed spatial-expression pattern signals.

73. (Previously Presented) An apparatus as set forth in claim 72, wherein:

the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

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74. (Currently Amended) A computer program product for analyzing gene expressions, the computer program product comprising means, encoded in a computer-readable medium for:

5 determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;
 forming a first spatial-expression pattern by:
 selecting a chromosomal region having a length and an exon having a start and a stop position;
 associating the gene expression within the first gene expression pattern with its corresponding exon, ~~by:the corresponding exon having a length such that the gene expression is associated with the entire length of the corresponding exon~~;
 determining, within the chromosomal region, the start and stop
10 position of the exon; and
 associating the gene expression to the first-spatial expression pattern for the length between the start and stop position of the exon; and
 creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern
15 where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

75. (Original) A computer program product as set forth in claim 74, further comprising an means for:

20 identifying first regular spatial patterns in the first spatial-expression pattern signal.

76. (Withdrawn) A computer program product as set forth in claim 75, wherein
 the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal
25 processing.

77. (Original) A computer program product as set forth in claim 75, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

5 78. (Original) A computer program product as set forth in claim 74, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

10 selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern with its corresponding exon.

79. (Original) A computer program product as set forth in claim 78, further comprising 15 acts of:

identifying first regular spatial patterns in the first spatial-expression pattern signal;

identifying second regular spatial patterns in the second spatial-expression pattern signal; and

20 comparing the first and second regular spatial patterns.

80. (Original) A computer program product as set forth in claim 78, further comprising acts of:

comparing all formed spatial-expression pattern signals.

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81. (Previously Presented) A computer program product as set forth in claim 80, wherein:

the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.